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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2834.52 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-4
Perfect score: 1101
Sequence: 1 atgaagttcttacttactac.....caggtgttcagaanaataa 1101

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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13: gb_un:*
14: gb_vl:*
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16: em_fun:*
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32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
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37: em_hcg_vrt:*
38: em_gv:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219	19.9	828	3	AB045179
2	217.4	19.7	808	3	AB045178
3	214.2	19.5	840	3	AB045172
4	213.4	19.4	710	3	AB045171
5	210.4	19.1	780	3	AB045168
6	208.4	18.9	774	3	AB045170
7	202	18.3	784	3	AB045167
8	201.2	18.3	781	3	AB045165
9	194.8	17.7	785	3	AB045177
10	194.2	17.6	1443	8	FSOKCH
11	194.2	17.6	1473	6	A21795
12	194.2	17.6	1473	6	A23637
13	194.2	17.6	1473	6	A23646
14	194.2	17.6	1473	6	A23955
15	194.2	17.6	1473	6	A23959
16	194.2	17.6	1473	6	A41660
17	194.2	17.6	1473	6	AR072922
18	194.2	17.6	1473	6	BD002249
19	194.2	17.6	1473	6	BD010853
20	194.2	17.6	1473	6	113885
21	194.2	17.6	1473	6	121317
22	194.2	17.6	1473	6	157984
23	191.2	17.4	759	3	AB045174
24	189.4	17.2	783	3	AB045173
25	188.6	17.1	761	3	AB045175
26	188.2	17.1	802	3	AB045176
27	187.6	17.0	798	3	AB045166
28	186.2	16.9	785	3	AB045169
29	181.2	16.5	1423	6	AR094309
30	178	16.2	927	6	AR094307
31	177.8	16.1	960	6	AR094305
32	177.8	16.1	1132	6	AR094315
33	177.2	16.1	924	6	A68074
34	177.2	16.1	924	6	AR163169
35	176.8	16.1	894	6	AR094306
36	174.4	15.8	919	6	A68072
37	174.4	15.8	919	6	AR163168
38	168.4	15.3	1418	8	PEQ277482
39	166.4	15.1	922	6	A68070
40	166.4	15.1	922	6	AR163167
41	166	15.1	1154	6	AR094308
42	163.8	14.9	913	6	AR094311
43	162	14.7	885	6	AR094316
44	161.6	14.7	912	6	A68076
45	161.6	14.7	912	6	AR163170

ALIGNMENTS

RESULT 1
AB045179
LOCUS
DEFINITION Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA,
AB045179
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AB045179 828 bp mRNA linear INV 14-PEB-2001
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
cellulase homologue, clone:6-47, complete cds.
AB045179.1 GI:8926990
Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA,
clone:6-47.
Reticulitermes speratus hindgut symbiont 130484
1 (sites)
Ohkoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
Diverse genes of cellulase homologues of glycosyl hydrolase family

45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
2102023
2 (bases 1 to 828)

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory, Hiroshima
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkumamailman.riken.go.jp, Tel.66-48-467-9545,
Fax:66-48-462-4672)

FEATURES

source
Location/Qualifiers
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/organism="Reticulitermes speratus hindgut symbiont
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RT"

BASE COUNT 231 a 133 c 208 g 256 t
ORIGIN

Query Match 19.9%; Score 219; DB 3; Length 828;
Best Local Similarity 62.8%; Pred. No. 2e-47;
Matches 396; Conservative 0; Mismatches 220; Indels 15; Gaps 3;

474 TGTACAGTGTCTACTGCTGTTAGGATGCTGTAAAGCCTCTGACGCGCG 533
Db TGTATCTGGAGGACTACGCTTATTTGGATTTTTCGAAAGCTCATGATGAGAAA 132
Qy 534 TTAGCCCAATGCTGCTCTCTGCAAGTCTGTAAACAAGATGATGATGCTGCTT-- 551
Db 133 AAAACCTGCTGACTGACCTGTTGATGCTGTGAAAGATGGACAAAGACCTTGC 192
Qy 592 -AGTACAGCAATGTCCAAAGTGTGTAAAGTGTGTAAACATTAATGTGTAAACAA 650
Db 193 AAGCAATGACACAGTAAATGAGTGTGTGCGGAGATGATGATGATGATGATGATG 252
Qy 651 CCAGCTTGGCTGTAAAGTATATCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 710
Db 253 AGCACAATGGCTGTATATGATGATGATGATGATGATGATGATGATGATGATGATG 309
Qy 711 TGTGTGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 770
Db 310 TGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 369
Qy 771 TGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 830
Db 370 GAATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 424
Qy 831 TGTGTGCTACTTGAATGCAATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 890
Db 425 ----AACCAATTTGATCTTGCAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 891 CAGCAATGGGCTCTCCCAATGACGCTTGGGCTGAGATTCGATGATTTTCTTCTG 950
Db 481 TCAGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540
Qy 951 ATCTGATGCTGTAGTCTTCTTCCGACATCCAGCTGTGTGTGTGTGTGTGTGTGTGT 1010
Db 541 TTCTAATGTTCTCAATCTCTTCTGCTTCCAGCTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 1011 GTTCAAGAGCTGATTAACCAAGCAATGATTAACAAGAGTGTGTGTGTGTGTGTGTGT 1070
Db 601 GTTCAAAATGCTGACCACTTCATCAATTTCAACCAAGTGAATGCCAATGATTT 660

Qy 1071 CACCGCCAGACAGTGTCTTCAAGAAATTA 1101
Db 661 GATGCAAGAACCAATTCAGAACTACTTA 691

RESULT 2
AB045178
LOCUS
DEFINITION
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
cellulase homologue, clone:45-6, complete cds.
AB045178
AB045178.1 GI:8926988

ACCESSION
VERSION
KEYWORDS
SOURCE
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
clone:45-6.
Reticulitermes speratus hindgut symbiont 130484
Unclassified.

ORGANISM
REFERENCE
AUTHORS
TITLE
1 (sites)
Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
Diverse genes of cellulase homologues of glycosyl hydrolase family
45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory, Hiroshima
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkumamailman.riken.go.jp, Tel.66-48-467-9545,
Fax:66-48-462-4672)

FEATURES

source
Location/Qualifiers
1..808
/organism="Reticulitermes speratus hindgut symbiont
130484"
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BASE COUNT 199 a 148 c 207 g 254 t
ORIGIN

Query Match 19.7%; Score 217.4; DB 3; Length 808;
Best Local Similarity 62.1%; Pred. No. 5.4e-47;
Matches 362; Conservative 0; Mismatches 221; Indels 12; Gaps 2;

487 ACTACTGCTTATGAGATGCTGTAAAGCCTCTGATGCTGCGCCGCTAAGCCCATGTC 546
Db 88 ACACTGCTTATGAGATGCTGTAAAGCCTCTGATGCTGCGCCGCTAAGCCCATGTC 147
Qy 547 AGTTCTCGTCAAGTCTGTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
Db 148 TCCAGCCGCTGTACATGTGCAAAAGATGCAAACTGCAAGTGTGCAACAGCGCAAA 207
Qy 607 CAAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 666
Db 208 TCAGCTGCAATGAGCGGACAGCATVATGTGTATGATCAACACCGCTGTCTGTC 267
Qy 667 AACGATTAATCTGCTATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
Db 268 AATGATCATATGCAATGGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
Qy 727 TGTGTGCTTCTGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 786

Db 472 ACAGCTCATCTGGGCTCTGCTGATGTGGGAAAGTCGTATGAGGGGTCTCTCC 531
 Oy 949 GCATCTGCTGCTCTAGTCTTCTCTCCGACTCCAGCTGTTGTAATGAGATTCAAC 1008
 Db 532 CGCAGTGAATCTCCGACCTCTCTGGGCTCTTCAGGCTGCTGCGACGTGAGATTTCAT 591
 Oy 1009 TGGTTCAAGAAGCGGTGATTAACCAAGCATGACTTCAAGAAAGTTACTGTCACAGGAA 1068
 Db 592 TGGTTCCAAATGCCGACATCCGTCATGAATTAACGTGTGTCTGCTGCCCAAGTAG 651
 Oy 1069 ATCAACGCCCAAGACAGGTTGTTCAAGAAATA 1100
 Db 652 TTGATTCGCAAAACCAATTGACAGACGCAATTA 683

RESULT 6
 AB045170 774 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:8-38, complete cds.
 AB045170
 ACCESSION AB045170.1 GI:8926972
 VERSION
 KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-38.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 UNCLASSIFIED.
 REFERENCE 1 (sites)
 AUTHORS Ohoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 774)
 AUTHORS Ohkuma,M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hirotsawa 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
 FEATURES
 SOURCE Location/Qualifiers
 1. 774
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 BASE COUNT 179 a 144 c 212 g 239 t
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 Best Local Similarity 61.7%; Pred. No. 14e-44;
 Matches 389; Conservative 0; Mismatches 226; Indels 15; Gaps 3;

Oy 475 GGTAAACGGTGTCACTACTGTTATGAGATTGCTTAAGGCTCTCTAGCTGCGCCGCT 534
 Db 97 GATACCTGCAGAAACCCGTTATGGGATTGCTCAAGAAAGATTGGCTGGAGAG 156
 Oy 535 AAGGCCATGTCAGTTCTCTGCTCAAGTCTGTAACAAAGATGCTGACTGCCCTT--- 591
 Db 157 AAGGCTATGTGACAAACCTATTGATGCTGCGCAAAAGATGTACCAACAGAGTTCA 216

Oy 592 AGTACAGCATATGTCCAAAGTGGCTGTAAACGGTGTAAACATTAATGTGTACAGAAC 651
 Db 217 AGCAACGACACCGTTAATGATCAGGCTGTGATGGCGAGATGATATATGTATTAGTCA 276
 Oy 652 CAGCTTGGGCTGTAAACGATTAATCTGCTTATGCTTGGCTGCTGCTGCATCAGTGT 711
 Db 277 TCTCCGTTGGGGTGTCAATGATTTCTTTGCTTGGGTTTGGCTGCGACCGGTTCAAG 336
 Oy 712 GGTGTGAATCTGCTGGTGTGCTGTTCTTTGCACTTACTTACTTACCTGCT 771
 Db 337 GGTAGAGCGCTGCC---TGTGCAATGTATTACAGATTACATTCATCTTGGCCAGTT 393
 Oy 772 GCTGTAAAGATGATGTTATCCAAAGTCACTAACAATGCTGTGATCTTGGCTCTACT 831
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 Oy 832 GGTGCTCATTTGACTTGCATTAATGCCGCTGCTGTGTTGTTGTTCAATGCTTCTCC 891
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 Oy 892 AAGCAATGGGGTGTCCCAATGACGTTGGGGCTCGAGATACGGGTGATTTCTTCTGCA 951
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 Oy 1012 TTCAAGAACGCTGATTAACCAAGCATGACTTCAAGAAAGTTACTGTCACAGAAATC 1071
 Db 625 TTCCAGAACGCTGATTAATCCGTCATCAGCTTCAACGCTGTTGCTGTCTTACGACTGG 684
 Oy 1072 ACCGCCAAGACAGGTTGTTCAAGAAATA 1101
 Db 685 ATTCGAAACCAACCTGACGCTTTAA 714

RESULT 7
 AB045167 784 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:8-16, complete cds.
 AB045167
 ACCESSION AB045167.1 GI:8926966
 VERSION
 KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-16.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 UNCLASSIFIED.
 REFERENCE 1 (sites)
 AUTHORS Ohoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 784)
 AUTHORS Ohkuma,M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hirotsawa 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
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 RN"

BASE COUNT 202 a 153 c 210 g 219 t
 ORIGIN

Query Match 18.3%; Score 202; DB 3; Length 784;
 Best Local Similarity 61.1%; Pred. No. 7e-43;
 Matches 385; Conservative 0; Mismatches 230; Indels 15; Gaps 3;

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 Db 72 TCACGTGGCAAAACACAGCGCTATTGGACCTTTGCAAGAGGTCTCTGCTGGAGAC 131
 Qy 534 TAAGCCCAATGCTGCTCTCTGCAAGTCTGTACCAAGATGCTGCTGCTCTT-- 591
 Db 132 AAAGCCCATGTTAGCAAGCCCATGACACATGCGGAAGAGGACACACAGATGTC 191
 Qy 592 -AGTACAGCAATGTCACAAAGTGTGTAAAGTGTGTAAAGTGTGTAAAGTGTGTAA 650
 Db 192 AAGCAACGACACCGTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 251
 Qy 651 CAAGCTTGGCTGTAAAGATATCTGTGCTATGTTGCTGCTGCTGCTGCTGCTGCTG 710
 Db 252 AACACCGTGGGCTGTAAATGATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCT 308
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 Db 309 AAGAGGCGAAGAGCCGATGCTGCAACGTGTAAAGTGTGTGTGTGTGTGTGTGTGT 368
 Qy 771 TGTGTGTAAGATGTTATCAAGTCACTAAGTGTGTGTGTGTGTGTGTGTGTGTGT 830
 Db 369 CAATGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423
 Qy 831 TGTGTGCTCACTTATGCAATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 890
 Db 424 ----AACCAATTTATCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
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 Db 480 AGCTAAGT 539
 Qy 951 ATCTGACTGCTGT 1010
 Db 540 CAGCGAATGCTCTCACTCTCTCAAGGTCTTCAAGCTGCTGCTGCTGCTGCTGCTGCT 599
 Qy 1011 GTTCAAGAGCTGATTAACCAAGCATGATGATTAAGAGATGATGATGATGATGATG 1070
 Db 600 GTTCAAAATGCAACATGCTGCTCAATGATGATGATGATGATGATGATGATGATG 659
 Qy 1071 CACGCCCAAGACAGTGTGTCAAGAAATTA 1100
 Db 660 GATTGCGAAGCAATGTCAGACGCAATTA 689

RESULT 8
 AB045165 781 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:2-54, complete cds.
 ACCESSION AB045165
 VERSION AB045165.1 GI:8926962
 KEYWORDS

SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
 clone:2-54.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 UNCLASSIFIED.

REFERENCE
 AUTHORS Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Ueami, R. and Kudo, T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family

45 from the symbiotic protists in the hindgut of the termite
 Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 JOURNAL MEDLINE 21020023
 REFERENCE 2 (bases 1 to 781)
 AUTHORS Ohkuma, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
 Physical and Chemical Research), Microbiology Laboratory, Hiroshima
 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
 Fax:66-48-462-4672)

FEATURES
 SOURCE location/Qualifiers
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 130484"

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 WMSRYGVSSRSECSQIPSLQNGCCMRDPMQANDNPSINPNVSCPSBLIANTNCR
 RN"

BASE COUNT 193 a 143 c 210 g 235 t
 ORIGIN

Query Match 18.3%; Score 201.2; DB 3; Length 781;
 Best Local Similarity 61.5%; Pred. No. 1.e-42;
 Matches 380; Conservative 0; Mismatches 223; Indels 15; Gaps 3;

Qy 487 ACTACGCTGATTTGGAGATGCTGTGAAGGCTCTGATAGCTGCGCGGTAAGCCCAATGTC 546
 Db 82 ACAACCCGGTACTGGATGCTGCTGCAAGAGATGTTGGGATGGAACCAAGCTGATGTA 141
 Qy 547 AGTTCTCTGTCAAGTCTGTAAACAAAGTGTGTCACTGCTT--AGTACAGCAAT 603
 Db 142 ACGAGCCCTATTGATACATGTGCGAAGAGTGCACAAAGATGTCAAAGTAAAGATAGC 201
 Qy 604 GTCCAAAGTGTGTAAAGTGTGTAAAGTGTGTAAAGTGTGTAAAGTGTGTAAAGTGT 663
 Db 202 GTTAAATCCGGCTGTGATGTGAGGAAAGATATGATGATGATGATGATGATGATGAT 261
 Qy 664 GTTAAAGATATCTGCTGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
 Db 262 GTCAATGATTTCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 321
 Qy 724 CGCTGTGCTGTTCTTGTGTGAATCTTCACTTCACTTCACTTCACTTCACTTCACTT 783
 Db 322 GCTTGTGC--CACTGTACGAATGATGATGATGATGATGATGATGATGATGATGATG 378
 Qy 784 ATGTTATCAAGTCACTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
 Db 379 ATGATGTTCAAGTTACTTAACACTGCGGGGCACTTGTGTTCC-----AACCACTT 429
 Qy 844 GACTTGAAGATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
 Db 430 GATCTTGTCTATTCAGAGGGGATGATGATGATGATGATGATGATGATGATGATGATG 489
 Qy 904 GCTCCCAATGACGTTGAGGCTGCAATACGTTGATGATGATGATGATGATGATGATGAT 963
 Db 490 GCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 549
 Qy 964 AGCTTCTCTGCGACATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1023
 Db 550 CAGCTTCATAGATGCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATG 609
 Qy 1024 GATTAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1083
 Db 610 GATTAATCCGTCATCACTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 669

[illegible]

QY	DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	FEATURES	BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	372;	Conservative	Score	194.2;	DB	8;	Length	1443;	Indels	15;	Gaps	2	523
318	GGTCTTGCTGTGCTGCTGATTAATTGACATTTCAACAAGTGGCCGGTCAACGAAAGCAT	377																															
784	ATGCTTATCCAAAGCAGCTAACAACGTGTCGTGATCTCTGCTACTGCTGACACTT	843																															
378	ATGATGTGTTCAAAATPAACCAACAGGGGGTATCTAGGCTCC-----AATCAATTT	428																															
844	GACTTGCMAATAGCCCGGTGTGTGTGTGTGTATTTTCAATGCTGTCTCCAAACAATGGGGT	903																															
429	GATCTTGCGCATTTCCGGGGTGTGTGGGTTCGGATTTTACAACGGATGACCGCCCAATCGGGT	488																															
904	GCTCCCAATGACGGTGTGGGCTCGAGATACGGTGTGATTTCTTTCGATCTGACTGCTCT	963																															
489	GCTCCTTCAGATGTTGGGGAAGCCGGATATGAGGTGTTTCATCAAGAATGAATGCTCT	548																															
964	AGTCTTCTCTCCGACACTCCAGCTGTGTGTAAATGAGATTCACATGCTTTCAAGAACCT	1022																															
549	CAGCTTCATAGAGACTGACAGCTGTGATGCGCAGATGGAATTTGATTTGTTCCAGAACCT	608																															
1024	GATTAACCAACATGACTTATCAAGGAAGTTACTGTCCCAAGGAATACCGCCCAAGACA	108																															
609	GACATTCGGAACATCAATTTTACGACAGTGTATGATGTCACAGCTGAGATTATTTGCCAAATCC	668																															
1084	GGTTGTTCAAGAAATTA 1101																																
669	AATTGCACACCGAGTTTA 686																																
FSOCH	1443 bp	mRNA	linear	PLN 28-APR-1995																													
LOCUS	Fusarium oxysporum K-family cellulase homologue mRNA, complete cds																																
DEFINITION	Fusarium oxysporum K-family cellulase homologue, complete cds																																
ACCESSION	L29381																																
VERSION	L29381.1																																
KEYWORDS	GI:520822																																
SOURCE	K-family cellulase homologue; cellulase; homologue.																																
ORGANISM	Fusarium oxysporum																																
	Fusarium oxysporum																																
	Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;																																
	Hypocreales; mitosporic Hypocreales;																																

[illegible]

DB	668	TCGAC	TCGATTCGACATCAGTCGATG	1088
QY	1064	AGGAATCACC	CGCCAGACAGGTTG	1088
DB	728	AGGCTTCCTCGACATCAGTCGATG	752	
RESULT	12			
A23637				
LOCUS	A23637	1473 bp	mRNA	linear
DEFINITION	F. oxysporum endoglucanase gene.			
ACCESSION	A23637			
VERSION	A23637.1			
KEYWORDS	endoglucanase.			
SOURCE	Fusarium oxysporum			
ORGANISM	Fusarium oxysporum			
REFERENCE	Eukariotica; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.			
AUTHORS	1 (bases 1 to 1473)			
TITLE	Convents A.C., Busch, A. and Baeck, A.C.			
JOURNAL	Detergent compositions with high activity cellulase and softening clays			
FEATURES	Patent: EP 0495258-A 3 22-JUL-1992;			
SOURCE	THE PROCTER & GAMBLE COMPANY			
	Location/Qualifiers			
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BASE COUNT 343 a 453 c 337 g 340 t

Query Match 17.6%; Score 194.2; DB 6; Length 1473;
Best Local Similarity 59.5%; Pred. No. 8.3e-41;
Matches 372; Conservative 0; Mismatches 238; Indels 15; Gaps 2;

OY 464 GTGGTGCCTCTGTAAGCGGTCTCACTACTGTTATTGGGATTGCTTAAGGCTCTCTGTA 523
DB 143 GTGCTGCTCTGTAAGCGGTCTCACTACTGTTATTGGGATTGCTTAAGGCTCTCTGTA 202
OY 524 GCTGCGCGGTAAAGCGCAATGTCTCTCTCTCAAGTCTCTTAACAAGATGATGTA 583
DB 203 CTTGAGAGGAAAGGCTGCTCAACGCCCTGCTTAACCTTGATGAAGAACCAACC 262
OY 584 CTGCGCTTAAGTACAGCAATGTCCAAAGTGTGTAACGTTGTAACATGTGTA 643
DB 263 CCAATTTCCAAACCAATGTCTCAACGTTGTGAAGGTGTGATGCTTATGCTTGA 322
OY 644 ACGAACACAGCTTGGGCTGTAACGATTAATCTTGGCTATGTTGCTGCTGCTGCA 703
DB 323 CCAACTACTCTCTCTGCGGCTGTAACGATGAGCTTGGCTTACGCTTACCTTCAAGA 382
OY 704 TCAAGTGTGTAAGTAAATCTCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 763
DB 383 TCTCCGGTGTCCGAGGCGCAAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 442
OY 764 CCTCTGTGCTGTAAGTAAATGTATTCACAGTCACTAAGCTGTGCTGTGCTGTGCT 823
DB 443 GCCCGGTCAAGGCGCAAGTATGATGCTCAAGTCAACCAACGTAAGTATCTCGGC 501
OY 824 CCTCTACTGTGCTCACTTGAATGCAATGCCGCGGTGTGCTGTGCTGTGCTGTGCT 883
DB 502 -----GACAAACACTTCAATCTCATGATGCTCGGCGGTGTGCTGTGCTGTGCT 553
OY 884 GTTGTCTCAAGCAATGGGCTGCTCCCAATGACGTTGGGCTCGAATACGCTGTATTT 943
DB 554 GCTGCACTCTGAGTTGG-----CAAGGCTCTCGGCGGTGCCAAGTACGCGGTATCT 607
OY 944 CTCTGCACTGACTGCTCTAGTCTTCTTCCGCACTCCAAAGCTGTGTAATGAGAT 1003
DB 608 CCTCCCGAAGGAATGTATGATACCTCCGAGCTTCTCAAGGACGGTGTGCCATGCGAT 667
OY 1004 TCAACTGTGTAAGTAAAGTGTATTCACAGTCACTAAGTAAATTTACCTGTCCA 1063
DB 668 TCGACTGTGTAAGTAAAGTGTATTCACAGTCACTAAGTAAATTTACCTGTCCA 727
OY 1064 AGGAATACCGCCCAAGCAGTTG 1088
DB 728 AGGCTCTCTGACATCAAGTGAATG 752

RESULT 13
A23646 1473 bp mRNA linear PAT 23-FEB-1995
LOCUS A23646 F. oxysporum endoglucanase gene.
DEFINITION A23646
ACCESSION A23646
VERSION A23646.1 GI:832892
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum

REFERENCE
AUTHORS 1 (bases 1 to 1473)
TITLE Conventen,A.C., Buech,A. and Baeck,A.C.
JOURNAL Deletgent compositions with high activity cellulase and quaternary ammonium compounds
Patent: EP 0495554-A 3 22-JUL-1992;
THE PROCTER & GAMBLE COMPANY
FEATURES
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BASE COUNT 343 a 453 c 337 g 340 t

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OY 464 GTGGTGCCTCTGTAAGCGGTCTCACTACTGTTATTGGGATTGCTTAAGGCTCTCTGTA 523
DB 143 GTGCTGCTCTGTAAGCGGTCTCACTACTGTTATTGGGATTGCTTAAGGCTCTCTGTA 202
OY 524 GCTGCGCGGTAAAGCGCAATGTCTCTCTCTCAAGTCTCTTAACAAGATGATGTA 583
DB 203 CTTGAGAGGAAAGGCTGCTCAACGCCCTGCTTAACCTTGATGAAGAACCAACC 262
OY 584 CTGCGCTTAAGTACAGCAATGTCCAAAGTGTGTAACGTTGTAACATGTGTA 643
DB 263 CCAATTTCCAAACCAATGTCTCAACGTTGTGAAGGTGTGATGCTTATGCTTGA 322
OY 644 ACGAACACAGCTTGGGCTGTAACGATTAATCTTGGCTATGTTGCTGCTGCTGCA 703
DB 323 CCAACTACTCTCTCTGCGGCTGTAACGATGAGCTTGGCTTACGCTTACCTTCAAGA 382
OY 704 TCAAGTGTGTAAGTAAATCTCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 763
DB 383 TCTCCGGTGTCCGAGGCGCAAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 442
OY 764 CCTCTGTGCTGTAAGTAAATGTATTCACAGTCACTAAGCTGTGCTGTGCTGTGCT 823
DB 443 GCCCGGTCAAGGCGCAAGTATGATGCTCAAGTCAACCAACGTAAGTATCTCGGC 501
OY 824 CCTCTACTGTGCTCACTTGAATGCAATGCCGCGGTGTGCTGTGCTGTGCTGTGCT 883
DB 502 -----GACAAACACTTCAATCTCATGATGCTCGGCGGTGTGCTGTGCTGTGCT 553
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DB 608 CCTCCCGAAGGAATGTATGATACCTCCGAGCTTCTCAAGGACGGTGTGCCATGCGAT 667
OY 1004 TCAACTGTGTAAGTAAAGTGTATTCACAGTCACTAAGTAAATTTACCTGTCCA 1063
DB 668 TCGACTGTGTAAGTAAAGTGTATTCACAGTCACTAAGTAAATTTACCTGTCCA 727

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